

ConCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17, Search time 19.7133 Seconds
(without alignments)
58.517 Million cell updates/sec

Title: us-09-856-070-21

Perfect score: 60

Sequence: 1 EELMLRLQDYEE 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9634422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR1*

2: PIR2*

3: PIR3*

4: PIR4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	581	2 145889	ezrin - bovine
2	60	100.0	586	1 A34400	ezrin [validated]
3	60	100.0	630	2 T47177	hypothetical prote
4	57	95.0	596	1 H41129	ezrin - mouse
5	39	65.0	250	2 H84212	hypothetical prote
6	39	65.0	405	2 H36340	alpha(1,3)-fucosyl
7	39	65.0	594	2 S75044	hypothetical prote
8	39	65.0	880	2 F75104	conserved hypotet
9	39	65.0	1263	2 T15406	hypothetical prote
10	39	63.3	86	2 F97544	hypothetical prote
11	38	63.3	130	2 H84133	hypothetical prote
12	38	63.3	150	2 G97449	hypothetical trans
13	38	63.3	150	2 AF2667	transcription regu
14	38	63.3	1058	2 S65460	apolipoprotein B
15	38	63.3	1400	2 T22644	hypothetical prote
16	37	61.7	111	2 T12857	hypothetical prote
17	37	61.7	281	2 F75276	hypothetical prote
18	37	61.7	303	1 A55502	cheA activity-modu
19	37	61.7	306	2 T04932	2,3-dihydroxybiphe
20	37	61.7	421	2 B82832	protein export mem
21	37	61.7	337	1 A70364	conserved hypotet
22	37	61.7	454	2 S01092	fodrin alpha chain
23	37	61.7	756	2 T00367	hypothetical prote
24	37	61.7	1305	2 A64465	hypothetical prote
25	37	61.7	2472	2 A37316	ledrin alpha chain
26	37	61.7	2477	1 S1C8A	spectrin alpha cha
27	36	60.0	250	2 H83344	conserved hypotet
28	35	58.3	293	2 H84790	probable adenylylat
29	35	50.0	304	2 F50721	synovial chicken

ALIGNMENTS

RESULT 1

145889

ezrin - bovine

C:Species: Bos primigenius taurus (cattle)

C.Date: 15 Oct 1996 #sequence_revision: 15-Oct-1996 #text_change: 13-Aug-1999

C.Accession: 145889

R:Berenson, C M.; Zhao, H.; Saljoh, K.; Duman, R.S.; Nestler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A>Title: Ezrin and osteosarcoma, two proteins associated with cell shape and growth, a

A.Reference number: 145889

A.Accession: 145889

A>Status: preliminary; translated from GH/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1 581 <BER>

A:Cross-references: GH:M98498; NIH:q289407; PIR:AAA30510.1; PID:q289408

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

F:7-231/Domain: 1-116 3 1-membrane binding domain homology: 841.

Query Match 100.0%; Score 60; DB 2; Length 581;

Best Local Similarity 100.0%; Pred. No. 0.0092;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12

DB 345 EELMLRLQDYEE 456

RESULT 2

A34400

ezrin [validated] - human

N:Alternate names: cytoovillin; p81 protein; villin 2

C:Species: Homo sapiens (man)

C.Date: 22-Jun-1990 #sequence_revision: 14-Jul-1994 #text_change: 08-Dec-2000

C.Accession: A34400; S09263; F61002

R:Teramachi, O.; Wistqvist, P.; Pakkaneen, R.; Grzeschik, K.H.; Wahlstrom, T.; Vaheri, A.

J. Biol. Chem. 265, 16727-16732, 1989

A>Title: Cytoovillin, a microvillar Mr 75,000 protein, cDNA sequence, prokaryotic exp

A.Reference number: A34400; MIM:444694; PMID:2574149

A.Accession: A34400

A.Molecule type: mRNA

A.Residues: 1-596 <IUP>

A:Cross-references: GB:J05021

A>Note: the translation of residues 1-11 is not given

A>Note: parts of this sequence were confirmed by protein sequencing

R:Gould, K.L.; Brutscher, A.; Esch, F.S.; Hunter, I.

EMBO J. 8, 4133-4142, 1989

A>Title: cDNA cloning and sequencing of the protein tyrosine kinase substrate, ezrin,

A.Reference number: S09263; MIM:444694; PMID:2591371

A.Accession: S09263

A.Molecule type: mRNA

A.Residues: 2-586 <IUP>

A:Cross-references: GH:M51521; NIH:q1282; PIR:CAA38833.1; F01g31283

huntingtin-associa
huntingtin-associ
ethylamine phosph
conserved hypotet
ethanolamine-phosp
hypothetical prote
probable PING fine
DNA polymerase 1 p
alpha-actinin 1 -
probable ubiquitin
Pholius-luciferin
Rhodinus luciferin
hypothetical prote
hypothetical prote
ABC transport prot

30 36 60.0 317 2 S67493
31 36 60.0 329 2 S72555
32 36 60.0 327 2 T42499
33 36 60.0 338 2 G82554
34 36 60.0 365 2 T37720
35 36 60.0 621 2 G83474
36 36 60.0 630 2 T02524
37 36 60.0 880 2 I63680
38 36 60.0 892 1 FAHUA
39 36 60.0 1108 2 T41188
40 35.5 59.2 547 2 S62787
41 35.5 59.2 548 2 S33788
42 35.5 59.2 550 1 A26772
43 35 58.3 66 2 A84093
44 35 58.3 152 2 T36984
45 35 58.3 218 2 S75100

Riba, G.; Kasimsson, H.H.; Van Den Hulck, M.; Van Hamme, J.; Puype, M.; Gassel, H.; C. Electrophoresis 11, 528-546, 1990

A:Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing.

A:Reference number: A61002-M010-0101404; PMID:1666755

A:Accession: E61002

A:Molecule type: protein

A:Residues: 255-263;194,'Q',196,199,'X',201,264,270, HAD-

A:Note: It is not certain whether this material represents carin or radixin (see entry A

A:Note: This material corresponds to transformed epithelial amnion cell (AMA) database B

C:Comment: This protein is located in microvilli and is proposed to play a role in modu

C:Genetics:

A:Gene: GPH;Vil2

A:Cross-references: GPH:120489; OMIM:123900

A:Map position: 6q25-6q26

C:Superfamily: carin; protein 4.1 membrane binding domain homolog

C:Keywords: actin binding; cytoskeleton; membrane-associated protein; phosphoprotein

F:2-586/Product: carin #status experimental #MAT

F:7-291/Domain: protein 4.1 membrane binding domain homolog #B412

F:753-586/Region: actin binding #status predicted

F:66/Binding site: phosphate (Ser) (covalent) #status predicted

F:214,299,342/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0% Score 60; DB 1; Length 586;

Best Local Similarity 100.0%; Pred.No. 0.0993;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12

10 445 EELMLRLQDYEE 356

|||||

RESULT 3

T47177

hypothetical protein DKFZp762H157.1 human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Apr-2000 #sequence-revision 20-Apr-2000 #text-change 02-Sep-2000

C:Accession: T47177

R:Ottowald, H.; Obermaier, H.; Mewes, H.W.; Weill, H.; Wilmann, S.

A:Note: This material corresponds to transformed epithelial amnion cell (AMA) database B

A:Reference number: 224177

A:Accession: T47177

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-630;AAA

A:Cross-references: EMBL:AL162086

A:Experimental source: adult melanoma (Mewes cell line); clone DKFZp762H157

C:Genetics:

A:Note: DKFZp762H157.1

C:Superfamily: carin; Protein 4.1 membrane binding domain homolog

Query Match 100.0% Score 60; DB 2; Length 630;

Best Local Similarity 100.0%; Pred.No. 0.01;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12

10 389 EELMLRLQDYEE 400

|||||

RESULT 4

R41129

carin - mouse

N:Alternate names: cytovillin; p81 protein; radixin; villin 2

C:Species: Mus musculus (house mouse)

C:Date: 04-Aug-1992 #sequence-revision 14-Jul-1994 #text-change 22-Feb-1999

C:Accession: R41129; C46561; A46561; M46561; S24290

R:Fukuyama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.

A:Cell Biol. 115, 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.

A:Reference number: A41129; M010-0206460; PMID:1955455

A:Accession: R41129

A:Molecule type: mRNA

A:Residues: 1-586;FUN-

A:Cross references: EMBL:U06071; NID:q150880; PDB:CAA43086.1; PDB:q50881
 R:Experiment, M.; Burgess, W.H.; Chan, D.; Braker, D.J.; Bretscher, A.; Samuelson, L.E.
 J. Immunol. 149, 1847-1852, 1992
 A:Title: Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein in T ce
 A:Reference number: A46501; MUID:92388649; PMID:1381389
 A:Accession: C46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Molecular type: protein
 A:Residues: 412-426 <EGE>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112948)
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Molecular type: protein
 A:Residues: 27-33, E' <EGE>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112946)
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 51-57, 148, L' 150, G' 152-155 <EGS>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112940)
 C:Comment: This protein is located in microvilli and is proposed to play a role in mo
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosph
 F:2 586/Product: ezrin #status predicted <MAT>
 F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:553-586/Region: actin binding #status predicted
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted
 F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 95.0%; Score 57; DB 1; Length 586;
 Best Local Similarity 91.7%; Pred. No. 0.032;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12
 DB 345 EELMLRLQDYEQ 356
 |||||

RESULT 5
 H84212
 Hypothetical protein Vmg0546c [imported] Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Accession: H84212
 R:NU, W.V.; Kennedy, S.P.; Mahairas, G.G.; Herquist, H.; Pan, M.; Shukla, H.D.; Lasky
 Jung, K.H.; Alam, M.; Freitas, J.
 Proc Natl Acad Sci U S A 97, 12176-12181, 2000
 A:Authors: Abd, S.; Daniels, C.J.; Dennis, F.P.; Omet, A.E.; Elhardt, H.; Lowe, T.M.;
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: H84212
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <STON
 A:Cross references: GB AE064437; NID:q1508145; PDB:AAI9068.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VMC0546C
 C:Superfamily: 3 isopropylmalate dehydratase leuB chain

Query Match 65.0%; Score 39; DB 2; Length 250;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12
 DB 226 EGVVSLQDMEE 237
 |||||

RESULT 6

B36340

alpha(1,4)-fucosyltransferase (EC 2.4.1.) 4 precursor [validated] - human
 Alternate names: CD15; ELAM-1 ligand fucosyltransferase (ELFT); FC3A; FUC-TIV; myeloid
 C:Species: Homo sapiens (man)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

A:Accession: B36340; A:Accession: A40976; A41202

R:Goal: S.E. Hession, C. Goll, D. Griffiths, R. Tizard, R. Newman, B. Chi-Rosso,

Cell 63, 1349-1356, 1990

A:Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.

A:Reference number: A36340; MIM:102044

A:Accession: B36340

A:Molecule type: mRNA

A:Residues: 1-405 <GOEL>

A:Cross-references: GR-M5806; NID:q182068; PID:AAA6172 1; PID-q182069

A:Accession: A36340

A:Molecule type: mRNA

A:Accession: A36340

A:Residues: 1-86, 107-108, 105-106

A:Cross-references: GR-M5806; NID:q182070; PID:AAA6173 1; PID-q182071

A:Note: the codon used as an initiator for this translation is not in a good context for

R:Low, J.B.: Kukowska-Latallo, J.F.; Nair, P.P.; Larsen, P.D.; Marks, P.M.; Macher, B.A.

J. Biol. Chem. 266, 17447-17477, 1991

A:Title: Molecular cloning of a human fucosyltransferase gene that determines expression

A:Reference number: A40976; MIM:117630; PMID:1176630

A:Accession: A40976

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86, 107-108, 105-106

A:Cross-references: GR-M5806; NID:q182751; PID:AAA6277 1; PID-q182729

R:Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.

J. Biol. Chem. 266, 21777-21783, 1991

A:Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but does

A:Reference number: A41202; MIM:6204084; PMID:1171893

A:Accession: A41202

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-240, 242-400 <KIM>

A:Cross-references: GR-M5806; NID:q259005; PID:AAA6049 1; PID-q239006

C:Genetics:

A:Gene: GDB:FUT4; CD15; FC3A; FUC-TIV

A:Cross-references: GDB:131563; OMIM:104230

A:Map position: 11q21-11q21

C:Superfamily: galactoside 3(4)-L-fucosyltransferase

C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

F.1-48/bmain: signal sequence #status predicted <STC>

F.49-405/product: alpha(1,3) fucosyltransferase 4 #status predicted <MAT>

F.91,190/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.0% Score 39; DB 2; Length 405;

Best Local Similarity 66.7% Pred. No. 32;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12

II III IIII

DB 136 EEDVLRVLDYEE 147

RESULT 7

S75944

hypothetical protein - Synchocystis sp. (strain PCC 6803)

C:Species: Synchocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-2000

A:Accession: S75944

P:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, I.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis

A:Reference number: S74322; MIM:47061201; PMID:8905241

A:Accession: S75944

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-584 <KAN>

A:Cross-references: EMBL:D04006; GB:A5001349; NID:q1001291; PID:BAAL0791.1; PID:q100

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 65.0% Score 39; DB 2; Length 584;

Best Local Similarity 63.8% Pred. No. 47;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 11

II III IIII

DB 521 EELSLRLQDYEE 531

RESULT 8

F75103

conserved hypothetical protein PAH0812 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001

A:Accession: F75103

P:Anonymous; Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence. Insights into archaeal chromosome s

A:Reference number: A75001

A:Accession: F75103

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-880 <KAW>

A:Cross-references: GB:AJ248286; GB:AI090836; NID:q5458366; PID:CA850131.1; PID:q545

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAH0812

C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 65.0% Score 39; DB 2; Length 880;

Best Local Similarity 66.7% Pred. No. 73;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12

II III IIII

DB 589 EELMLRLQDYEE 600

RESULT 9

T15496

hypothetical protein G14F5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 29-Sep-1999

C:Accession: T15496

R:Minx, P.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid G14F5.

A:Reference number: Z18361

A:Accession: T15496

A>Status: preliminary; translated from CH/EMBL/DDHJ

A:Molecule type: DNA

A:Residues: 1-1263 <MIN>

A:Cross-references: EMBL:D20082; NID:q861384; PID:q861385; PID:AAA52402.1; CESP:G14F

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:G14F5.3

A:Accession: T15496

A:Residues: 1-1263, 1265-1267, 1269-1270, 1272-1273, 1275-1276, 1278-1279, 1281-1282, 1284-1285, 1287-1288, 1290-1291, 1293-1294, 1296-1297, 1299-1300, 1302-1303, 1305-1306, 1308-1309, 1311-1312, 1314-1315, 1317-1318, 1320-1321, 1323-1324, 1326-1327, 1329-1330, 1332-1333, 1335-1336, 1338-1339, 1341-1342, 1344-1345, 1347-1348, 1350-1351, 1353-1354, 1356-1357, 1359-1360, 1362-1363, 1365-1366, 1368-1369, 1371-1372, 1374-1375, 1377-1378, 1380-1381, 1383-1384, 1386-1387, 1389-1390, 1392-1393, 1395-1396, 1398-1399, 1401-1402, 1404-1405, 1407-1408, 1410-1411, 1413-1414, 1416-1417, 1419-1420, 1422-1423, 1425-1426, 1428-1429, 1431-1432, 1434-1435, 1437-1438, 1440-1441, 1443-1444, 1446-1447, 1449-1450, 1452-1453, 1455-1456, 1458-1459, 1461-1462, 1464-1465, 1467-1468, 1470-1471, 1473-1474, 1476-1477, 1479-1480, 1482-1483, 1485-1486, 1488-1489, 1491-1492, 1494-1495, 1497-1498, 1499-1500, 1501-1502, 1503-1504, 1505-1506, 1507-1508, 1509-1510, 1511-1512, 1513-1514, 1515-1516, 1517-1518, 1519-1520, 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C97449
hypothetical transcription regulator y4D [imported] - Agrobacterium tumefaciens (strain C-8)
C-Species: Agrobacterium tumefaciens
C-Disease: 30-Sep-2001 accession=11743194
C-Accession: C97449
A-Cooditor: B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, R.; Goldmeyer, A.; Liu, F.; Wolam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A-Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A-Reference number: A97359; PMID:11743194
A-Accession: C97449
A-Status: preliminary

Best local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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DB 1013 KFTQIKLHDYEE 1024

RESULT 15
T22644
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C:Date: 15-Oct-1999 #sequence_revision 15 Oct-1999 #text_change 15-Oct-1999
C:Accession: T22644
R:Lennard, N.
submitted to the EMBL Data Library, July 1996
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Query Match 63.3%; Score 38; DB 2; Length 1400;
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Search completed: January 16, 2003, 16:57:51
Job time : 20.7143 secs

